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GenCore version 5.1.6 , Copyright (c) 1993 - 2003 Compugen Ltd.
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nucleic search, using frame\_plus\_p2n model

OM protein

Run on: August 29, 2003, 09:51:49; Search time 2055 Seconds (without alignments) 1596.644 Million cell updates/sec

1596.644 Million cell upda

Title: US-09-866-582A-2
Perfect score; 661
Sequence: 1 MDAVDRGVYFDEDFHVRILD......GEQELMIQKLSDSSGAAYV 135
Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Xgapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 22781392 segs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Listing first 100 summaries

Command line parameters:
-MODEL=frame+\_pZn model -DEV=xlp
-MODEL=frame+\_pZn model -DEV=xlp
-MODEL=frame+\_pZn model -DEV=xlp
-CgnZ\_1/USPTO\_spool\_p/US0986682/runat\_27082003\_095333\_9839/app\_query.fasta\_1.327
-DB=EST -QFWT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-blts -START=1 -END=-1 -MATRIX-blosum62 -TRANS=human40 cdi -LIST=100
-DOCALIGN=200 -THR\_SCORE=pCt -THR\_MAX=100 -TRR\_MIN=0 -ALIGN=50 -MODE=LOCAL
-OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINIEN=0 -MAXIEN=20000000
-USER=US09866582\_eCGN 1\_1\_2874\_erunat\_27082003\_095333\_9839 -NCPU=6 -ICPU=3
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THRRADS=1 -XGAPDP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

EST:\*

Database :

1: em\_estba:\*
2: em\_esthum.\*
3: em\_estin:\*
4: em\_estin:\*
5: em\_estrov:\*
6: em\_estp::\*
7: em\_estp::\*
17: em\_estp::\*
10: gb\_est1:\*
11: gb\_hc:\*
11: gb\_est2:\*
11: gb\_est3:\*
11: gb\_est3:\*
11: gb\_est3:\*
11: em\_est5m::\*
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13: em\_est5m::\*
14: em\_est5m::\*
16: em\_est5m::\*
17: em\_gss\_hum:\*
18: em\_gss\_hum:\*

em\_gss\_pro:\* em\_gss\_rod:\* em\_gss\_phg:\*

em\_gss\_mus:,

em\_gss\_vrt:\* em\_gss\_fun:\* em\_gss\_mam:\* em\_gss\_vrl:\* gb\_gssl:\*

. 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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	Description	837 AV392837	30429 BW280429	30674 BW28067	26060 BP02606	15694 BW21569	13658 BP01365	08971 BP00897	13621 BW31362	79944 BW07994	988	7451 BW0//45	763 AV897763	L2507 BW312507	3735 NISC_ng	2 2	727	35126 BY63512	9080	3426 AV899426	18613 BW24861	999	1/926 BW11/92	594 cm54f10.w	34392 6015056	3692 UI-R-AB1	200	3561 UI-R-BUO	39218 UI-R-DK	52868 ur3/brz 5584 wiescos	0881 EST21682	76762 ih70c01	787	3522 LO	51938 AGENCOU	77210 A	70290 H	10927 U	77222 U	745.	3347 Mus musc	26846 ut88d02	36260 uf76e04.	/6815 1D/1CU2. 74751 BX274751	34690 ih70c01.	11517 pglln.p	1/180 6041/225 59785 BX259785	0 AV882930	9809 603159
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BE352290 493 bp mRNA linear EST 18-JUL-2000 894059C02.xl C. reinhardtii CC-1690, normalized, Lambda Zap II
Chlamydomonas reinhardtii cDNA, mRNA sequence.
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Chlamydomonas reinhardtii
Eukaryota, Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
(Loases 1 to 493)
Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P.,
McDermott, J. P., Silflow, C., Stern, D. and Surzyoki, R.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicallular System for Analyzing Gene Function and Regulation in
Unpublished
            /dev_stage="photoautotrophic growth"
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/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
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Tel: 919 613 8164
Fax: 919 613 8177
Email: chlamy@duke.edu.
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BF075368 224346 MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                       603109966
                                                                                                                                                                           BG101052 uy18908.y
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BX419276 BX419276
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Sato,S., Fukuzawa,H. and Tabata,S.
A large scale structural analysis of cDNAs in a unicellular green
alga, Chlamydomonas reinhardtii. I. Generation of 3433
DNA Res. 6 (6), 369-373 (1999)
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BU074070 in28c01.
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
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                                                             BU412690 6
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BU357913
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Kazusa DNA Research Institute
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL MEDLINE PUBMED

COMMENT

FEATURES

DEFINITION

RESULT 1 AV392837 LOCUS

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BW280674 Satch unpublished cDNA library, gonad Ciona intestinalis cDNA clone cigd014j07 5', mRNA sequence.
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1 (bases 1 to 653)
Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
Expressed genes in Ciona intestinalis (2002c)
                                                                                                                                                                                                                                                                                                                                        63 GGGCTTCATTTTGACGAAGTTAACAAGCTCAGAGTTTTAAAACCAGACACTAATCAGCAG 122
                                                                                                                                                                                                                                                                                                                                                                                                          183 CTTGTTGGTAGCTTCATAGAGATGACCGACGCANTCGCAAAAGATGTTGAAAATGAGAAA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluLeuGluArgLeuGlnMet 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 GluGluGlnSerLeuIleLysValLysGlyGluGluGluLeuMetIleGlnLysLeuSer 126
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107 c 121 g 194 t 1 others
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Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
1-18-175-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
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Department of Zoology
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                                                                                                                         Anote="Vector: pBluescript II SK-; Site_1: ECORI; Site_2:
XhOI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAPP (acetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in the
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
POLYA MRNA was purified from each sample, pooled and cDNA
synthesized. The CDNA was directionally cloned into lambda
ZAP II (Stratagene) in the EcoRN (5') and XhOI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with ExAssist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bwzsuq29 646 bp mRNA linear EST 11-NOV-2002 BW280429 Nori Satch unpublished cDNA library, gonad Ciona intestinalis cDNA clone cigd013n23 5', mRNA sequence.
                                                                                           /clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
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Eukaryota: Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 646)
Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
Expressed genes in Ciona intestinalis (2002c)
Unpublished
Contact: Nori Satoh
Department of Zoology.
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    .493
/organism="Chlamydomonas reinhardtii"

                                   /mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
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Conservative:
Mismatches:
Indels:
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Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:7719"
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Fax: 81-75-705-1113
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1 (bases 1 to 540)
Inaba,K., Padma,P., Satouh,Y., Shin-i,T., Kohara,Y., Satoh,N. and
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/tissue_type="gonad"
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| 108 c 121 g 196 t 3 others
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/db_xref="taxon:7719"
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Contact: Kazuo Inaba
Asamushi Marine Biological Statio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Asamushi, Aomori, Aomori 039-3501, Tel: 81-17-752-3394 Fax: 81-17-752-2765 Email: inaba@biology.tohoku.ac.jp.
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14-MAR-2002 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona. 1 (bases 1 to 541) Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T. Expressed genes in Ciona intestinalis 7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla 26 SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46 67 LeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLys 86 /clone="cits42a19"
/tissue\_type="testis"
/clone\_lib="K. Inaba unpublished cDNA library, testis"
101 c 102 g 147 t lothers LeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLys AV964246 Nori Satoh unpublished cDNA library, egg Ciona intestinalis cDNA clone cieg17g02 5', mRNA sequence. AV964246 540 41 34 47 0 Matches: Conservative: Email: satoh@ascidian.zool.kyoto-u.ac.jp. Location/Qualifiers /organism="Ciona intestinalis" /mol\_type="mmsNA" /db\_xref="taxon:7719" /clone="cieg17902" Mismatches: Indels: Sākyo-ku, Kyoto, Kyoto 606-8502, Japan Tel: 81-75-753-4081 Fax: 81-75-705-1113 ength: Gaps: US-09-866-582A-2 (1-135) x BP026060 (1-540) AV964246.1 GI:19453942 Unpublished Contact: Nori Satoh Department of Zoology 4.01e-08 200.00 61.48% 33.61% Ciona intestinalis Ciona intestinalis Kyoto University 127 AspSer 128 443 ACTTCT 448 Best Local Similarity: σ Percent Similarity: Alignment Scores:



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195
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Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 565)
Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
Expressed genes in Ciona intestinalis (2002c)
Unpublished
Contact: Nori Satoh
Department of Zoology
Kyoto University
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/tissue_type="whole animal"
/dev_stage="egg"
/clone_lib="Nori Satoh unpublished cDNA library, egg"
97 c 103 g 153 t
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/mol_type="mRNA"
/db_xref="taxon:7719"
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Tel: 81-75-753-4081
Fax: 81-75-705-1113
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Satoh, N., Satou, Y., Kohara, Y. and Shin-1, T.
Expressed genes in Ciona intestinalis
Contact: Nori Satoh
Department of Zoology
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/dev_stage="egg"
/clone_lib="Nori Satoh unpublished cDNA library, egg"
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Location/Qualifiers
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Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
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Fax: 81-75-705-1113
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/clone="ciad50e21"

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1 (bases 1 to 670)

Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.

Expressed genes in Ciona intestinalis
Unpublished
                                                                                                                                                                                                                                                                                                                                                                98
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/clone_lib="Nor! Satoh unpublished cDNA library, young
                                                                                                                                                                                                                                                        SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satch@ascidian.zool.kyoto-u.ac.jp.
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BP008971.1 GI:19500448
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Department of Zoology
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Ciona intestinalis
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BW298785
BW298785 Nori Satoh unpublished cDNA library, neural complex Ciona intestinalis cDNA clone cinc003m02 5', mRNA sequence.
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(bases 1 to 60)

Satou, Y., Shin-ig., Kohara, Y. and Satoh, N.

Expressed genes in Ciona intestinalis (2002c)

Unpublished

Contact: Nori Satoh

Department of Zoology

Kyoto University

Sakyo-ku, Kyoto, Kyoto 606-8502, Japan

Tel: 81-75-753-4081

Fax: 81-75-705-1113
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Location/Qualifiers
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Best Local Similarity:
Query Match:
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CAACAACAGTTGAAAGCACTCATAGCGGAGAAGAAAACACAACTTGAGCGATTGAATGTG 351
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Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
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1 (bases 1 to 683)
Satou, Y., Shin-i,T., Kohara,Y. and Satoh,N.
Unpublished
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Mismatches:
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Tel: 81-75-753-4081
Fax: 81-75-705-1113
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/db_xref="taxon:7719"
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Department of Zoology
Kyoto University
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Best Local Similarity:
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MRNA linear EST 20-OCT-2002 BW079944 Nori Satch unpublished cDNA library, egg Ciona intestinalis cDNA clone rcieg080kl3 3', mRNA sequence. BW079944.1 GI:24181356
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Ciona intestinalis
Eukaryotta, Metazoa, Chordata, Urochordata; Ascidiacea, Enterogona;
Entebobranchia; Cionidae; Ciona.
1 (bases 1 to 715)
Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.
Expressed genes in Ciona intestinalis (2002c)
                                                                                                                                                                                                                                                                                                                                                                         63 GGGCTTCATTTTGACGAAGTTAACAAGCTCAGAGTTTTAAAAACCAGACACTAATCAGCAG 122
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Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
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Best Local Similarity:
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Percent Similarity:
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BW077451/c
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AUTHORS
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Phlebobranchia; Cionidae; Ciona.

1 (bases 1 to 719)

Satou, Y., Shin i, T., Kohara, Y. and Satoh, N.

Expressed genes in Ciona intestinalis (2002c)

Unpublished

Contact: Nori Satoh

Department of Zoology

Kyoto University
                                                                                                                                                                                                                                                                                                                                                                                                 549 CTTGTTGGTAGCTTCATAGAAATGACCGACACAATCGCAAAAGATGTTGAAAATGAGAAA 490
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/clone="rcieg080k13"
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/dev_stage="egg"
/clone_lib="Nori Satch unpublished cDNA library, egg"
113 c 115 g 252 t
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Matches:
Conservative:
Mismatches:
Indels:
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Fax: 81-75-705-1113
Email: satch@ascidian.zool.kyoto-u.ac.jp.
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/mol_type="mRNA"
/db_xref="taxon:7719"
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BW077451 Nori Satch unpublished cDNA library, egg Clona intestinalis cDNA clone rcieg072121 3', mRNA sequence.
BW077451 GI:24178863
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1 (bases 1 to 720)

2 stou, Y., Shin-i, T., Kohara, Y. and Satoh, N.

Expressed genes in Ciona intestinalis (2002c)
                                                                                                                                                                                                                                                                                                                                                                                                                                          608 ACATCTGAACTGAAAGAGGAATGCCACGAATTCGTCTCGAAAAATCGACCAGTTTCAAAAA 549
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                                                                                                                                                                                                                                                                                                                              GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla 26
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/clone_lib="Nori Satch unpublished cDNA library, neural
complex" 259 t
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Conservative:
Mismatches:
Indels:
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Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-76-1113
Email: satch@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:7719"
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/clone="rcinc003m02"
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Department of Zoology
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308 ACTICT 303
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AV897763 Nori Satch unpublished cDNA library, young adult Ciona intestinalis cDNA clone rciad50e21 3', mRNA sequence.
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|||::::: ::: ::::!|||||||||| :::
CAACAGTTGAAAGCACTCATAGCGGAGAAAAACACAACTTGAGCGATTGAATGTG 375
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Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
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117 c 130 g 241 t
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1 (bases 1 to 758)
Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.
Expressed genes in Ciona intestinalis
Unpublished
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Conservative:
Mismatches:
Indels:
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/mol_type="mRNA"
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Tel: 81-75-753-4081
Fax: 81-75-705-1113
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AV897763.1 GI:16886861
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Department of Zoology
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BW213159 Nori Satch unpublished cDNA library, egg Ciona litestinalis cDNA clone cleg072121 5', mRNA sequence.
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1 (bases 1 to '17.)
2 satou, Y., Shin-17.; Kohara, Y. and Satoh, N.
Expressed genes in Ciona intestinalis (2002c)
Unpublished
Contact: Nori Satoh
Department of Zoology
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/clone="rcieg072121"
/tissue_type="whole animal"
/dev_stage="egg"
/clone_lib="Nori Satoh unpublished cDNA library, egg"
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Mismatches:
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Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:7719"
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Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
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BW312507
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Medrayota: Metazoa: Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia: Cionidae; Ciona.
1 (bases 1 to 759)
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                                                                                                                                                                                                                                                                                  46
                                                                                                                                                                                                                                                                                                                                                                                     86
/clone="rciad50e21"
/tissue_type="whole animal"
/dev_stage="young adult"
/clone_lib="Nori Satoh unpublished cDNA library, young adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla
                                                                                                                                                                                                                                                                                   SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                     GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluLeuGluArgLeuGlnMet
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Matches:
Conservative:
Mismatches:
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Location/Qualifiers
1. .759
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Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Ciona intestinalis"
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                                                                  267
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61.48%
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Best Local Similarity:
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TITLE
JOURNAL
COMMENT
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Silurana tropicalis cDNA clone
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Silurana tropicalis
Silurana tropicalis
Bukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Silurana.
I (basea: 1 to 615)
NIH-XCG http://image.llnl.gov/image/html/xenopuslib_info.shtml.
National Institute of Child Health and Human Development, National Unpublished
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 GluGluGlnSerLeuIleLysValLysGlyGluGluLeuMetIleGlnLysLeuSer 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ::: |||||||||| ||| ::: ||||||| 354 CAACAGGTCTGAATTGAATTGATTGAATTCTCA 413
                                                                                                                                                                                                                                                                                                                                                                                                                               114 ACATCTGAACTGAAAGAGGAATGCCACGAATTCGTCTCGAAAATCGACCAGTTTCAAAAA 173
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                                                                      unpublished cDNA library, heart"
238 t
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cDNA Library Preparation:
CDNA Library Prayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
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41
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Matches:
Conservative:
Mismatches:
Indels:
/db_xref="taxon:7719"
/clone="ciht023e1"
/tissue_type="heart"
/clone_lib="Nori Satoh un
a 113 c 133 g 238
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IMAGE:5382476 5', mRNA sequence.
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AL649467 XGC-gastrula Silurana tropicalis cDNA clone TGas049d15 5',
                                                                                                                                                                                                                                                                         /dev_stage="neurula"
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/clone_lib="XGC_neurula"
/note="Vector: pC5107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from neurula.
EcoRI NotI cut cDNA was then ligated into pCS107 with
ECORI NotI cut at the 3, end and NotI at the 3, end."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 GAAAAATGAAGGCAATAGGTGCCCGGAACTTATTAAAATCTATAGCAAAGCAAAGAGAA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302 GCCCAGCAGCAGCAACTGTATGCCTTAATAGCAGAGAAAAATGCAACTAGAAAGGTGC 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 GlnGlyLeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAla 64
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                                                                        Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_LD: TNeu094a07.PicSP6
Sequencing prime: PICSP6
This sequence is from a Xenopus Gene Collection (XGC) library
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Silurana tropicalis
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                                      Hinxton, Cambridgeshire, CB10 1SA, UK
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                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:8364"
                                                                                                                                               constructed by Aaron M. Zorn.
Location/Qualifiers
1. .619
                                                                                                                                                                                                                                                            /clone="TNeu094a07
                                                           trop@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
AL649467
AL649467.1 GI:17658653
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198.00
62.30%
32.79%
29.95%
   Contact: Taylor R
                      Centre
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Query Match:
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AL649467
                                                                                                                                                                    FEATURES
   COMMENT
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/mol_type="mRNA"
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Rocky: Cloned unidirectionally. Primer: Oligo dT. Average
insert size 2.1 kb. Constructed by Invitrogen. Note: This
is a Xenopus Ggne Collection (XGC) library."
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Silurana tropicalis
Bukaryota: Metazoca; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia: Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Silurana.
1 (bases 1 to 619)
Taylor, R., Ashurst, J.L., Croning, M.D.R., Zorn, A.M. and Rogers, J. Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="Two.006k05"
/dev_stage="neurula"
/lab_nost="Escherichia coli DH10B"
/clone_lii="XG-neurula"
/note="Vector: pcS107; Site_l: EcoRI; Site_2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula. EcoRI notI cut cDNA was then ligated into pcS107 with EcoRI at the 5, end and NotI at the 3, end."
a 135 c 143 g. 155 t
                                                                                                                                            Silurana tropicalis (western clawed frog)
Silurana tropicalis
Silurana tropicalis
Silurana tropicalis
Subraryotas (hordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Silurana.
I (bases I to 640)
Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
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Email: trop@sanger.ac.uk
Sanger Xenopus tropfealis EST project 2001
Sanger Xenopus Tropfealis EST project 2001
TROPTCALIS.SEQUENCE.ID: TNeu006k05.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. 2orn.
Location/Qualifiers
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/organism="silurana tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
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1 (bases 1 to 629)

Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J. Sanger Kanopus tropicalis EST project 2001 (10_2001)

Unpublished
Contact: Huckle E
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                                                                                                                                                                                                                                       HINXCON, Cambridgeshire, CB10 15A, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
Sanger Xenopus Tropicalis EST project 2001
FROPICALIS_SEQUENCE_ID: TGas049415.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Asron M. Zorn.
Location/Qualifiers
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SOURCE

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BW150890 115 bp mRNA linear EST 03-NOV-2002 BW150890 Nori Satch unpublished cDNA library, gonad Ciona intestinalis cDNA clone rcigd013n23 3', mRNA sequence.
                                                                                                                                                                                                                                                      Brain Science Institute
encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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                                                                                                                                                 Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Michela Fagiolini and Takao K. Hensch (Laboratory for Neuronal Circuit Development Brain Science Institut RIKEN 2-1 Hirosawa, Wako-shi, Saitama 351-0198 Japan ) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="k430066M20"
/tissue_type="visual cortex"
/clone_lib="RIKEN full-length enriched, visual cortex"
70 c 120 g 94 t
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/mol_type="mRNA"
/strain="C57BL/63"
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Location/Qualifiers
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URL:http://genome-gsc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp,
Alzawa.K., Akimura.T., Arakawa.T., Carninci.P., Fukuda,S., Hirozane,T., Imotani.K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata.M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaxi,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
                                                                                                                                                                                                                   EST 15-DEC-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
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BY635126 RIKEN full-length enriched, visual cortex Mus musculus
cDNA clone K430066M20 3', mRNA sequence.
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Normalization and subtraction of cap-trapper-selected cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
                                                                                                                                                                                                                                                            CDNA clone K430066M20 3 BY635126
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us-09-866-582a-2.rst

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222
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BW286181. GI:24866792
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Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 LysGlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluLeuGluArgLeuGln 105 :::||||::::: ::: ::::||||||||||||
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Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 GlyLeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGlu 65
                                                                                                                                                                                      /organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="t-axon.7719"
/clone="rcigd013n23"
/tissue_type="gonad"
/clone_lib="Nori Satoh unpublished cDNA library, gonad"
125 c 108 g 255 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                    6 ArgGlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsn
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41
34
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            Conservative:
Mismatches:
Indels:
                                                                                                  Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satch@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
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Matches:
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Best Local Similarity:
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Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 GluGluGlnSerLeuIleLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSer 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47 LeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLys 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla 26
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/clone="cigd002d11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AV899426 AVE Satch unpublished cDNA library, young adult Ciona intestinalis cDNA clone rciad74m19 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 LeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLys
Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 633)
Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
Uppublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       633
40
47
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                Email: satoh@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                      /organism="Ciona intestinalis"
                                                                                                                                                         Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
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Matches:
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AV899426.1 GI:16888524
                                                                                                   Contact: Nori Satoh
Department of Zoology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.01e-07
196.00
61.48%
32.79%
29.65%
                                                                                                                                           Kyoto University
                                                                                                                                                                                                                                                            1. .633
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Best Local Similarity:
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Alignment Scores:
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BW156639/c
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AUTHORS
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JOURNAL
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BW248613.1 GI:24828531
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Cióna intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LysGluGlnGluArgMetLeuAlaGluLysGlnGluGluLeuGluArgLeuGlnMetGlu 107
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/clone_lib="Nori Satoh unpublished cDNA library, young
adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 ValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAlaSer
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                                                                                                                                                                                                                                                                                      3 others
                                                                                                                                                                                                                                                                                                                                         661
40
34
47
0
1 (bases 1 to 661)
Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.
Expressed genes in Ciona intestinalis
Unpublished
                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                    Email: satoh@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
1. 661
/organism="Ciona intestinalis"
/db_xref="taxon:7119"
/clone="rciad74m19"
                                                      Contact: Nori Satch
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                    238 t
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196.00
61.16%
33.06%
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TCT 297
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DB:
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VERSION
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                                                                                                                                                                                                                                                                                                                                        Pred. No.:
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    REFERENCE
AUTHORS
TITLE
JOURNAL
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BW248613
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                                                          COMMENT
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BW156639 Nori Satch unpublished cDNA library, gonad Ciona intestinalis cDNA clone rcigd002d11 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 GluGluGlnSerLeuIleLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSer 126
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                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="whole animal"
/dev_stage="tailbud embryo"
/clone_lib="Nori Satoh unpublished cDNA library, tailbud
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47 LeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLys 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLys 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 674)
Satou,Y., Shin-1,T., Kohara,Y. and Satoh,N.
Expressed genes in Ciona intestinalis (2002c)
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35
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Matches:
Conservative:
Mismatches:
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1. 674
1. 704
Anime"Ciona intestinalis"
//Mol_type="mRNA"
//db_xref="taxon:7719"
/clone"citb078f08"
                                                                                                                                                                                                                                   Email: satoh@ascidian.zool.kyoto-u.ac.jp
                                                                              Unpublished
Contact: Norl Satch
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 t
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Phlebobranchia; Cionidae; Ciona
1 (bases 1 to 674)
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196.00
61.48%
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Ciona intestinalis
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Phlebobranchia; Cionidae; Ciona.
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TITLE
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COMMENT
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BW117926 GI:24364591
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Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 430 CAACAACAGTTGAAAGCACTCATAGCGGAGAAGAAAAACACAACTTGAGCGATTGAATGTG 371
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.

1 (bases 1 to 718)
Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.
Expressed genes in Ciona intestinalis (2002c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            550 CTTGTTGGTAGCTTCATAGAAATGACCGACGCAATCGCAAAAGATGTTGAAAATGAGAAA 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99
                                                                                                                                                                                                                                                           /tissue_type="gonad"
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127 c 110 g 260 t
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                                                                                                                                                                                                                                                                                                                                        718
40
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47
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                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
                                                                                                                      Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoMeascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                        /organism="Ciona intestinalis"
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                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:7719"
/clone="rcigd002d11"
                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-866-582A-2 (1-135) x BW156639
                                                                                  Contact: Nori Satoh
Department of Zoology
Kyoto University
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                                                                                                                                                                                                                                                                                                                                                    196.00
61.48%
32.79%
29.65%
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BJ064012 NIBB Mochii normalized Xenopus tailbud library Xenopus laevis cDNA clone XL078b07 5', mRNA sequence.
BJ064012. GI:17424850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 GluGluGlnSerLeuIleLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSer 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::: ||||||||| ||| ::: |||||||| 368 CAACACCAGTCTTGAATTGATTGAATTGTCA 309
                                                                                                                                                                                                                                                                                                                                                                /tissue_type="whole animal"
/dev_stage="tailbud embryo"
/clone_lib="Nori Satoh unpublished cDNA library, tailbud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              742
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l (bases 1 to 742)
Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
Expressed genes in Ciona intestinalis (2002c)
Unpublished
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                     Email: satoh@ascidian.zool.kyoto-u.ac.jp.
                                                                                                                                                                                                                                                                              /organism="Ciona intestinalis"
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/clone="rcitb078f08"
                                                                                        Confract: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
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Xenopus laevis
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/sex="female"
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919 541-4571
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                               Xenopus laevis
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AW645594.1 GI:7403048
                                                         Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGCAAACAACCGAATTAAAGGAGGAGTGCCGAGATTTTGTAGACAAAATAGGACATTTT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |||| :::|||| :::|||| :::
245 CAGAAAGTAGTGGGGGGGACTAATTGAGCTTGTTGATGAGTTAGCTAAAGAAACCGAAAAC 304
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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                                                                                                                                                                                                                                                                                                                                /clone_lib="NIBB Mochii normalized Xenopus tailbud
library"
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                                                                                                             Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
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Matches:
Conservative:
Mismatches:
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/organism="xenopus laevis"
/mol.type="mRNA"
/db_xref="taxon:8355"
/clone="xL078807"
/tissue_type="whole embryo"
/dev_stage="stage 25"
                                                                                    Expressed genes in X. laevis embryo
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                                                                                                                                                                                                   Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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                                          (bases 1 to 548)
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485 TTTAAC 490
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DEFINITION
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lacyis egges. The strain was prepared in the vector prins solution and subtracted in the vector prins. With the vector prins. W. B. Normalization and subtraction: two approaches to facilitate gene discovery', Genome Research 6:791-806, 1996. The first strand synthesis used a Norl-driB primer; double stranded cDNAs were ligated to ECORI adapters, digested with NotI, and directionally cloned into the NotI and ECORI-digested prins. The library contained approximately 7.2 x 10.5 The library con
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                                                                                                                                                                                                             Xenopodinae; Xenopus.

1 (Bases I to 609)

1 (bases I to 609)

Jr. Moore,D.T., Lai,W.S., Thorn,J.M., Kennington,E.A., Staffa,N.G.
Jr., Moore,D.T., Bouffard,G.G., Beckstrom-Sternberg,S.M., Touchman
J.W., Bonaddo,M.F. and Soares,M.B.

The NIEMS Xenopus maternal EST project: interim analysis of the
first 13,879 ESTs from unfertilized eggs
21211403

21211403
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Office of Clinical Research and Laboratory of Signal Transduction
National Institute of Environmental Health Sciences
A2-05 NIEHS, 101 Alexander Drive, Research Triangle Park, NC 27709,
                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: black009@niehs.nih.gov
Clone is available through Research Genetics, Inc., 2130 Memorial
Parkway, Huntsville, AL 35901
phone 800-533-4363 ext.cdna, fax 256-536-9016 att:cdna, email
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Conservative:
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/dev_stage="unfertilized egg"
Xenopus laevis (African clawed frog)
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Plate: 0153 row: F column:
Seg primer: T7 primer.
Location/Qualifiers
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University of lowa 375 Mebber, lowa City, IA 52242, USA 7515 Mewton Road, 4156 MEBBE, lowa City, IA 52242, USA 761: 319 335 8256
Email: bento-soares@ulowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. CDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 03-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 285 AATGAAAAGATGAGCCATCGGTGCTCGGAACTTGCTCAAATCTATAGCAAAGCAGAGA 344
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                                                                                                                                                                                                                              105 GIGAAGCAGGGGCTACACTITGAIGAACIGAACAAGCIGAGGGIGIIGGACCCAGAGGII 164
                                                                                                                                                                                                                                                                                                                                                                                                     44 MetGlnGlyLeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGlu 63
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                       4 ValAspArgGlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLys
                                                                                                                                                                                                                                                                                                                                        165 ACCCAGCAGACCATAGAGCTGAAGGAAGAGTGCAAAGACTTTGTGGACAAAATTGGCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 AlaGluLysLeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI703692 427 bp mRNA linear EST 03-JUN-U1-R-AB1-yu-h-06-0-UI.s1 UI-R-AB1 Rattus norvegicus CDNA clone UI-R-AB1-yu-h-06-0-UI 3', mRNA sequence.
AI703692.1 GI:4991592
                                                                                                                                                                                                                                                                                       24 TyrAsnAlaSerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsn
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Coordinated Laboratory for Computational Genomics
0 0

    427
    organism="Rattus norvegicus"

Mismatches:
Indels:
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/strain="Sprague-Dawley"
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                                                            Gaps:
                                                                                                             US-09-866-582A-2 (1-135) x BE884392 (1-917)
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32.23%
29.50%
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   Similarity:
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/mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9607361"
/clone="ImAGE::3907361"
/tissue_type="leiomyosarcoma"
/tissue_type=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE884392 917 bp mRNA linear EST 20-OCT-2000 601505670F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3907361 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlnMetGluGluGlnSerLeuIleLysValLysGlyGluGluLeuMetIleGlnLys 124
                                                                                                                                                                                                                                                                                                                                                                                                                                      85 ArgLysGlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluLeuGluArgLeu 104
                                                                                                                                                                                                                                                                  CAGAAAGTAGTGGGTGGACTAATTGAGCTTGTTGATGAGTTAGCTAAAGAAACCGAAAAC 267
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NIH-WGC http://mgc.noi.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
      GlnGlyLeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAla
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                                                                                                                                                  CAGCAAACAACCGAATTAAAAGGAGGAGTGCCGAGATTTTTGTAGACAAAATAGGACATTTT
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37
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Matches:
Conservative:
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 642.
Location/Qualifiers
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TITLE
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//CLORGE_11be_"SCARCES_mammary_gland_NMLMG"
//CLORGE_11be_"SCARCES_mammary_gland_Nith a modified
//NOte="Vector: pT7T3D-Pac (Pharmacia) with a modified
//NOTES_VECTOR: pT7T3D-Pac (Pharmacia) with a modified root of the primed gland tissue from a lactating female, and was then primed with a Not I - Oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Scares and M. Fatima Bonaldo. "
12. c. 74 g 139 t
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BY438168.1 GI:26721595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            411 GAGGCAGGCTGCATTTTGATGAACTGAACAAGCTCCGAGTGTTGGACCCAGAGGTCACC 352
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                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:952545.
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41
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                          /sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
                                                                                                                                                                                                   /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                     /clone="IMAGE:1547197"
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                                                                                                                                                           Location/Qualifiers
                       Other_ESTs: ug64h07.y1
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61.83%
30.53%
29.43%
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Best Local Similarity:
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       /clone="UT-R-ABI-yu-h-06-0-UI"
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/lab_host="BH10B (Life Technologies)"
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/clone_lib="UT-R-ABI"
/note="Vector: p7730-Pac (Pharmacia) with a modified
/note="Vector: p7730-Pac (Pharmacia) with a modified
/note="Vector: p7730-Pac (Pharmacia) rith a unormalized library constructed from 16.5 dpc
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Lennon and Soares, Genome Research 6: 791-806, 1996.
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man of the provided by Jim Lin, Department of Biology,
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNas

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNas
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN Integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1171 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
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URL:http://genome-resels.
URL:http://genome-gsc.riken.go.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
"T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
"M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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COMMENT

/organism="Mus musculus"

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AW533561 432 bp mRNA linear EST 06-MAR-2000 UI-R-BU0-and-d-03-0-UI.sl UI-R-BU0 Rattus norvegicus cDNA clone UI-R-BU0-and-d-03-0-UI 3', mRNA sequence.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                          /tissue_type="kidney"
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/clone_lib="RIKEN full-length enriched, 17 days embryo
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University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
                                                                                                                                                                                                                                                  431
40
41
45
1
                                                                                                                                                                                                                                                                     Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ::: ||||||| :::::::: |||||||| 383 TTTATTTTCAGAAATGAACTGAAAATTTCAGT 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 LeuMetIleGlnLysLeuSerAspSerSerSer 130
                                                                                                                                                         ų
                                                                                                                                                         96
                                                                                                                                                                                                                                                  Length:
                                                                                                                                                                                                                                                                                                                                        Indels:
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                                                                                                                                                                                                                                                                                                                                                                  Gaps:
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="1920155K14"
                                                                                                                                                                                                                                                                                                                                                                                                          US-09-866-582A-2 (1-135) x BY438168 (1-431)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Norway rat)
Rattus norvegicus
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                                                                                                                                                                                                                                             9.96e-08
194.50
61.83%
30.53%
29.43%
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                                                                                                                                                         75 c
                                                                                                                                  kidney
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EST 19-JUL-2001

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/de__stage="Database" (Life Technologies)"
/lab_host="Database" (Life Technologies)"
/clone_lib="UI-R-DK0"
/clone_lib="WetCor: pT73D-Pec (Pharmacia) with a modified
polylinker; Site_l: Not I; Site_2: Eco RI; The UI-R-DKO
library is a subtracted library derived from a mixture of
five individually tagged normalized rat libraries:
brain-nRBP (20%), heart-nRPP (20%), kidney-nRKP (20%),
aorta-nRAP (20%), heart-nRPP (20%), sorta-nRAP (20%),
aorta-nRAP (20%), mod placenta-nRPP (20%), sorta-nRAP (20%),
aorta-nRAP (20%), and placenta-nRPP (20%), sorta-nRAP (20%),
advantage (20%), and placent developmental time-points:
embryonic day I7, adult day 12, adult day 75, and adult day 21,
adult day 1, adult day 12, adult day 75, and adult day
200. (Exception: the aorta pool does not contain embryonic
day 17 RNA and the placenta pool contains only the three
embryonic stages). Each library was normalized.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coordinated Laboratory for Computational Genomics
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 9256
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized rat kidney pool library CDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         individually according to the procedure described by Bonaldo, Lennon & Soares (Genome Research Genome 6: 791-806, 1996). For construction of the DKO subtracted library, plasmid DNA from each of the five individually tagged normalized libraries was mixed in the proportions specified above and electroporated into competent bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for production of single-stranded circular bNA representing the pool of libraries. Single-stranded circular DNA representing these five normalized libraries was then used as a tracer in a subtractive hybridization with a driver (PCR amplified inserts from a plasmid DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 434)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                             BI289218
UI-R-DKO-cfj-c-07-0-UI.sl UI-R-DKO Rattus norvegicus cDNA clone
UI-R-DKO-cfj-c-07-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UT-R-DKO-cfj-c-07-0-UI"
/dev_stage="ADULT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Rattus norvegicus"
56 TTTATTTTCAGAAATGAACTGAAAATTTCAGT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus
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                                                                                                                                                                                                                                                                      BI289218
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                                                                            RESULT 36
BI289218/c
                                                                                                                                                                                     DEFINITION
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MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
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                                                                                                                                                     LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="procedural color="10" |
/db_xref="procedural color="10" |
/dev_zstage="dault" |
/dev_zstage="dault" |
/dab_host="DHU0B (Life Technologies)" |
/clone_lib="UI-R-BU0" 
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                                                            Email: bench-soares@ulowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized ganglia library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             426 GAGGCAGGCCTGCACTTCGATGAGCTGAACATCGGGTGTTGGACCCAGAGGTTACC 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 ArgLysGlnLysGluGlnGlnArgMetLeuAlaGluLysGlnGluGluLeuGluArgLeu 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 GlnGlyLeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAla 64
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. 432
/organls="Rattus norvegicus"
/mol_type="mRRA"
/strain="Sprague-Dawley"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
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TAG_TISSUE-ganglia
                                                                                                                                                                                                                                                                                                                                                                               Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: M13 Forward POLYA=Yes.
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114 c
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61.83%
30.53%
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Best Local Similarity:
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AI256584.1 GI:3864109
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Best Local Similarity:
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VERSION
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                                                                                                          FEATURES
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template preparation) comprising: a) a set of about 1,000 arrayed clones from each of the five non-normalized libraries of brain (CTOS), heart (CSOS), kidney (CUOS), and placenta (CXOS). The resulting pool of approximately 5,000 clones represented about 33.3% of the final driver population. A set of about 2,000 arrayed clones from each of the five normalized libraries of brain (CTO), heart (CSO), kidney (CUO), acrta (CWO), and placenta (CXO). The resulting pool of about 10,000 clones represented about 66.6% of the final driver population. TAG_LIB-UI-F-DKO

TAG_LIB-UI-F-DKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        454 bp mRNA linear EST 21-JUN-2000 uf37b12.x1 Soares_mammary_gland_NNLMG Mus musculus cDNA clone IMAGE:1513535 3' similar to TR:Q61025 Q61025 HYPOTHETICAL 15.2 KD PROFIEIN. ;, mRNA sequence. BE132868 GI:8595368 EE132868.1 GI:8595368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 GCCCAGCAACAGCAACTGCAGGCACTGATAGCAGAAAAGAAGATGCAGCTAGAAAGGTAT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Musc. 1 (bases 1 to 454)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 GAGAAATGAAGGCCATTGGTGCTCGAAACTTGCTGAAATCCATAGCGAAGCAGAGAAA 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AsnAlaSerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMet
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                                                                                                                                                                                                                                                                                                   434
40
41
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 TITATITITCAGAAATGAACTGAAAATITCAGT 35
                                                                                                                                                                                                                                                                                                                                                                       Indels:
                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
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Unpublished
Other_ESTs: uf37b12.y1
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194.50
61.83%
30.53%
29.43%
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BE132868/C
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VERSION
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/organism="wus musculus"
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/db_xref="taxon:10090"
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/clone="IMAGE:151335"
/clone="IMAGE:151335"
/tissue_type="mammary gland"
/tote="vector: pring-pace (Pharmacia) with a modified
/note="vector tote of the Not I and Eco RI sites of the
modified pring: vector. Library is normalized. Library
was constructed by Banto Soares and M. Fatima Bonaldo."

1 and 127 c 78 g 148 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               558 CAGCAGACTGTGGAGCTCAAGGAGGAGTGCAAGGACTTTGTGGACAAAATTGGCCAGTTT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlnGlyLeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAla 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298 CAGAAAATTGTTGGTGGTCTAATTGAGCTTGTTGATCAGCTTGCCAAAGAAGCAGGAAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 AspargGlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLySTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 AsnAlaSerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMet
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:940387
High quality sequence stop: 414.
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Mismatches:
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Matches:
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                                                                                                                                                                             Location/Qualifiers
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194.50
61.83%
30.53%
29.43%
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AI170881 467 bp' mRNA linear EST 08-JAN-1999 EST216822 Normalized rat muscle, Bento Soares Rattus sp. cDNA clone RWUBC92 3' end, mRNA sequence.
AI170881.1 GI:4134559
                        GCCCAGCAGCAGCAGCAGCAGCAGCCCTGATAGCAGAAAAGAAGAGGCAGCAAGAAAGGTAT 132
                                                                                                                                                                       GlnMetGluGluGlnSerLeuIleLysValLysGlyGluGln-------Glu 119
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                                                                                     85 ArgLysGlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluLeuGluArgLeu 104
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                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (pases 1 to 467)
Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Normalized rat muscle, Bento Soares"
/note="Organ: muscle; Vector: pT7T3Pac; Site_l: EcoRI;
Site_2: NotI"
130 81 9 155 t
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Unpublished
On Oct 6, 1998 this sequence version replaced gi:3710921.
Contact: Lee, NH
The Institute for Genomic Research
7712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-5229
Fax: (301)-838-0208
Email: nhlee@tigr.org
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Mismatches:
Indels:
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Matches:
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/organism="Rattus sp."
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/db_xref="taxon:10118"
/clone="RMUBC92"
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Best Local Similarity:
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/dev_stage="adult"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Sugano mouse liver mlia"
/clone_lib="Sugano mouse liver mlia"
/clone_lib="Sugano mouse liver mlia"
/clone_logan: liver; Vector: pME185-FL3; Site_l: DraIII
(CACGTGTG); Site_2: braIII (CACGATGTG); Ist strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCTTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCTACTGG], digested
and cloned into distinct DraIII sites of the pME185-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the CDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTGCTCTAAAAGCTGCG and 3' end
primer CGACTGCAGCTACACACCA."
97 a 127 c 76 g 163 t
                                                                                                                                                                                              Waterston, P. Wilson, R. Dennon, G., Soares, B., Wilson, R. and Waterston, R. Materston, R. Materston, R. The WashU-HHMI Mouse EST Project
Contact: Marra Mywouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HMI Mouse EST Project
WashU-HMI Mouse EST Project
WashU-HMI Mouse EST Project
Fax: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1810
                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 463)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
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371 CAGCAGACTGTGGAGCTCAAGGAGTGCAAGGACTTTGTGGAAATTGGCCAGTTT 312
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Conservative:
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Location/Qualifiers
1. 463
/organism="Mus musculus"
/mol_type="mRRA"
./strain="C57BL"
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/clone="IMAGE:1889480"
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                      Mus musculus (house mouse)
Mus musculus
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61.83%
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29.43%
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Best Local Similarity:
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AUTHORS
KEYWORDS
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UI-R-DY1-cnu-j-06-0-UI.S1 UI-R-DY1 Rattus norvegicus cDNA clone
BQ208726
BQ208726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          366 CAGCAGACTGTGGAGCTCAAGGAGTGCAAGGACTTTGTGGACAAAATTGGCCCAGTTT 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 CGGGTTGAATATGAAGCTTTGTGTAAAGTAGAAGCAGAACAAAATGAATTTATTGACCAA 67
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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University of Iowa
Ty5 Newton Road 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565.
Email: bento-soares@ulowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first
oligo-dT priming.Size-selected by column fractionation; average insert size 1.06kb. Primary library, unamplified." 79 g 160 t 1 others
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                                       5 AspArgGlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyr
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40
41
41
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Matches:
Conservative:
Mismatches:
Indels:
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97044477
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BM876762 474 bp mRNA linear EST 12-MAR-2002 170Col.1.4. Melton Mouse El5 Fancaeas Library 2 M16B2 Mus musculus cDNA clone IMAGE:5681664 3' similar to TR:061025 Q61025 HYPOTHETICAL 15.2 KD PROTEIN. ; mRNA sequence.
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Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lenishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Schmitt, A., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Jackson, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.

Findocrine Pancreas Consortium
Unpublished
                                                                                                                                                                                                                      GCCCAGCAACAGCAACTGCAGGCACTGATAGCAGAAAAGAGAGATGCAGCTAGAAAGGTAT 110
                                                                                                                                     229 GAGAAAATGAAGGCCATTGGTGCTCGAAACTTGCTGAAATCCATAGCGAAGGAGAGAAA 170
                                                                                                                                                                                                                                                                                    GlnMetGluGluGlnSerLeuIleLysValLysGlyGluGln------Glu 119
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Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
                                          (browners, harvard edu)
MGI:1959542 This sequence now available from the IMAGE consortium, for clone orders contact: info@image.llnl.gov
                                                                                                                                                                                            ArgLysGlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluLeuGluArgLeu 104
                                                                                                    84
                                                                                                                                                                                                                                                                                                                               CGGGTTGAATATGAAGCTTTGTGTAAAGTAGAAGCAGAACAAAATGAATTTATTGACCAA 50
           GlnGlyLeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAla 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information o
Obtaining a clone please contact: Juliana Brown
                                                                                                    GluLysLeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLys
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/dev_stage="Embryonic day 16.5"
/lab_host="TOP10"
                                                                                                                                                                                                                                                                                                                                                                               120 LeuMetIleGlnLysLeuSerAspSerSerSer 130
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="ICR"
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High quality sequence stop: 466.
Location/Qualifiers
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AUTHORS
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us-09-866-582a-2.rst

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/MIDL_VPPE="INTURNA"
//Strain="CG7BL/6"
/db_xref="taxon:10090"
/clone="UI + DJ2-bub-d-13-0-UI"
/tissue_type="subfornical organ and postrema"
/dv_stage="Adult"
/lab_host="PH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="WIH_BMAP_DJ2"
/note="Organ: brain; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-M-DJ2 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is: GCTACATGAT, subfornical organ and area postrema.

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Bonaldo, M. F., Lennon, G. and Soares, M. B.
Normalization and subtraction: two approaches to facilitate gene
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         127 CGGGTTGAATATGAAGCTTTGTGAAGTAGAAGCAGAACAAAATGAATTTATTGACCAA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Chin, H
National Institute of Mental Health
National Institute of Mental Health
2001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-943, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
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TAG_SEQ=GCTACATGAT"
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Matches:
                                                                                                            /organism="Mus musculus"
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                      /organism="Rattus norvegicus"
/mol_type="mrna"
/mol_type="mrna"
/strain="Sprague-Dawley"
/db_xref="taxon:1016"
/clone="UI-R-DYI-cnu-j-06-0-UI"
/tlssue_type="Cartilage"
/dev_stage="ADULT"
/lab_b="UI-R-DYI"
/note="Organ: Femur and Tibia; Vector: pT7T3D-Pac
/clone_lib="UI-R-DYI"
/note="Organ: Femur and Tibia; Vector: pT7T3D-Pac
/clone_lib="UI-R-DYI"
/note="Corgan: Femur and Tibia; vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site= 1: Not I;
Site_2: ECO RI: UI-R-DYI is a normalized CDNA library
containing the following tissue(s): Rat Cartilage from
Femur and Tibia. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand CDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor: dispested with Not
I, and cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is CTAATGGACG. The Rat
cartillage tissue was provided by Dr Jeff Stevens at the
University of Towa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ::: ||||
367 CAGCAGACCACAGAGGTCAAGGAAGAGTGCAAGGACTTTGTGGGAAATTGGCCAGTTT 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     307 CAGAAAATCGTTGGTGGTCTGATTGAGCTTGTTGATCAGCTTGCCAAAGAAGCAGAAGAAC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 GAGAAAATGAAGGCCATTGGTGCTCGAAACTTGCTGAAATCCATAGCGAAGCAGAGAA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 ArgLysGlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluLeuGluArgLeu 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---Glu 119
strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized cartilage library ORNA Library Preparation: M.B. Clone distribution: clones will be available through Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 AsnAlaSerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMet
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Matches:
Conservative:

    .517
    /organism="Rattus norvegicus"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University of Towa.
TAG_LIB=UI-R-DYI
TAG_TISSUE-cartilage
TAG_SEQ-CTAATGGACG"
                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 g
                                                                                                                                                              Genetics (www.resgen.com)
Seg primer: M13 Forward
POLYA-Yes.
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29.43%
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Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

1 (Dases 1 to 573)

Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X., Grahovac,M.J., Pantano,S., Sano,Y., Piao,Y., Nagaraja,R., Doi,H., Wood,W.H.

Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray

Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW553522 ST3 bp mRNA linear EST 10-JUN-2003 L0228610-3 NIA Mouse Newborn Ovary cDNA Library Mus musculus cDNA AW553522 GI:31568866
                                                                                                                                                            807 CAGAAAATTGTTGGTGGTCTAATTGAGCTTGTTGATCAGCTTGCCAAAGAAGAAGCAGAAAC 248
                                                                                                                                                                                                                                                                                                                                                                                            85 ArgLysGlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluLeuGluArgLeu 104
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                                                                                                                                      5 AspArgGlyValTyrPheAspGluAspPheHisValArglleLeuAspValAspLysTyr 24
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                                                                                                                                                                                                                                                    CAGCAGACTGTGGAGCTCAAGGAGGAGTGCAAGGACTTTGTGGACAAAATTGGCCAGTTT
                                                                                                                                                                                                                                                                                             GlnGlyLeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAla
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Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Silte 4000, Baltimore, MD 21224-6820, USA
Email: cdnadlgsun grc.nia.nih.gov
Plate: L0228 row: C column: 10
Seq primer: -21M13 Forward
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On Mar 7, 2000 this sequence version replaced gi:7198945
        Conservative:
Mismatches:
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/mol_type="mRNA"
/strain="C57BL/GJ"
/db_xref="niaEST:L022BC10-3"
/db_xref="taxon:10090"
                                          Indels:
                                                                                                 US-09-866-582A-2 (1-135) x BQ174785 (1-539)
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High quality sequence stop: 573
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    61.83%
30.53%
29.43%
Percent Similarity:
Best Local Similarity:
Query Match:
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SOURCE
ORGANISM
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VERSION
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MEDLINE
PUBMED
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
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615 bp mRNA linear EST 21-OCT-2002
AGENCOURT_10617261 NIH_MGC_169 Mus musculus cDNA clone
IMAGE:6742597 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                   349 CAGCAGACTGTGGAGGTCAAGGAGGAGTTTGTGGACAAAATTGGCCAGTTT 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 GCCCAGCAGCAGCAGCAGGCCCTGATAGCAGAAAAAAAGAAGGCAGCTAGAAAGGTAT 110
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410
41
5
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Matches:
Conservative:
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/dev_stage="Newborn Ovary"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 TTTATTTTCAGAAATGAACTGAAAATTTCAGT
                                                                                                                                                                                                                                                                                                                         Indels:
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194.50
61.83%
30.53%
29.43%
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Query Match:
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27

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/clone="INGASINITYS".
/lab_host="INGASINITYS".
/lab_host="DH108 (phage-resistant)"
/clone=lib="NHH MGC_ldd"
/clone=lib="NHH MGC_ldd"
/note="Vector: pCMV-SPORT6"
Not1; Non-normalized full-length enriched library from pooled mouse embryonic limb, maxilla and mandible, day 10.5 and 11.5 (size selected for the 0.5-1 kb fragments) cloned directionally, priming method: Oligo-dT. cDNA enrichment: >lk bp, Average insert size 1.8k bp. Priming sequence: 5 GACTAGTTCTAGATCGCGAGGGGGCGCCC(T) 3'. Tissue contributed by, David Rowe: Library constructed by ResGen, Invitrogen Corp."
Invitrogen Corp."
                                                                                                                                                                                EST 06-JAN-2003
    265 CAGCAGACTGTGGAGCTCAAGGAGGAGTGCAAGGACTTTGTGGACAAAATTGGCCAGTTT 324
                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus I (bases 1 to 633)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 GlnGlyLeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAla 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bloscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: NDAMOGG row: b column: 02

High quality sequence stop: 633.
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                                                                                                                                                                         CA977210
AGENCOURT_11292396 NIH_MGC_164 Mus musculus cDNA clone IMAGE:30147961 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. David Rowe and Dr. Mina
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Matches:
Conservative:
Mismatches:
                                                                                                   560
                                                                                           528 TTTATTTTCAGAAATGAACTGAAAATTTCAGT
                                                            120 LeuMetIleGlnLysLeuSerAspSerSerSer
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                               Mus musculus (house mouse).
Mus musculus
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CA977210.1 GI:27509864
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AUTHORS
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                                                                                                                                                         CA977210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Confect: Robert Strausberg, Ph.D.
Email: Ggapbs-remail.nih.gov
Tissue Procurement: Dr. Jonathan Kuo, NIMH
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
from through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLCM3080 row: o column: 12
High quality sequence stop: 540.
Location/Qualifiers

cee 1. 615
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228 CAGCAGACTGTGGAGCTCAAGGAGTGCAAGGACTTTGTGGACAAATTGGCCAGTTT 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 GlnMetGluGluGlnSerLeuileLysValLysGlyGluGln--------Glu 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85 ArgLysGlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluLeuGluArgLeu 104
                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 615)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 AspArgGlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyr 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 GlnGlyLeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAla 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 GluLysLeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLys
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/clone="IMAGE:6742597"
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                                        musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
    BU961938:1 GI:24191510
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194.50
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                                        Mus musculus
Mus musculus
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Best Local Similarity:
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directionally into pT7T3-Pac vector. The oligonucleotide
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H3085G04-3 NIA Mouse 15K cDNA Clone
H3085G04 3', mRNA sequence.
BG070290
BG070290.1 GI:12552859
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                                                                                                                                                                                                              220
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                                                                                                                                                    TAG_LIB=UI-R-EPO
TAG_TISSUE=duodenum
TAG_SEQ=TGTGGTTCAT"
a 165 c 136 g
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Best Local Similarity:
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/dev_stage="ADDLT"
/dev_stage="ADDLT"
/dab_host="DHIOB (Life Technologies)"
/dab_host="DHIOB (Life Technologies)"
/clone_lib="UT-R-EDO"
/note="Vector: PT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_l: Not I; Site_l: Eoc RI, UI-R-EDO is a
subtracted cDNA library constructed according to Bonaldo,
Lennon and Soares, Genome Research, 6:791-806, 1996. First
strand cDNA synthesis was primed with an oligo-dr primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
                                                                                                                                                                                                                                                                                                                                                                                                      EST 02-MAY-2002
                                                                                                                                                                                                      105 GlnMetGluGluGlnSerLeuIleLysValLysGlyGluGln-------Glu 119
|||| :::|||| :::|||| CAGAAAATIGTIGGTGGTGGTTGCTGCCAAAGAAGCAGGAAC 384
                                                                           85 ArgLysGlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluLeuGluArgLeu 104
                                                                                                                                                                                                                                    Email: benco-soares@ulowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized duodenum library CDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  approaches to facilitate gene
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UI-R-EPO-COG-b-22-0-UI.S1 UI-R-EPO Rattus norvegicus CDNA clone
UZ-R-EPO-COG-b-22-0-UI 3', mRNA sequence.
                                                                                                                                                                  445 GCCCAGCAGCAGCTGCAGGCCCTGATAGCAGAAAGAAGACGCAGCTAGAAAGGTAT
                                                     GluLysLeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University of Iowa
775 Newton Road , 4156 MEBRF, Iowa City, IA 52242,
781: 319 335 9250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                                                   LeuMetIleGlnLysLeuSerAspSerSerSer 130
                                                                                                                                                                                                                                                                                                                     565 TTTATTTTCAGAAATGAACTGAAAATTTCAGT 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 672)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two appr

    .672
    /organism="Rattus norvegicus"

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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Norway rat)
Rattus norvegicus
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Seq primer: M13 Forward
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Tanaka, T.S., Jardat, S.A., Lim, M.K., Kargul, G.J., Wang, X., Grahovac, M.J., Pantano, S., Sano, Y., Piao, Y., Nagaraja, R., Doi, H., Wood, W.H. III. Becker, K.G. and Ko, M.S.H.
Genome-wide expression profitling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
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Set Mus musculus cDNA clone
used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are distal colon, GAAGTGCTCC; osteoblast, AAGATACAA; cell line R3327 5A, GGACTAGATC; cell line R3327 5P, CACGTGAGAT; duodenum, TGTGGTTCAT; prostate,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||| :::||| :::||| cagaaaatcgttggtcgttgttgatcagcttgccaaagaagcagagaac 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 GAGGCAGGGCTGCACTTCGATGAGCTGAACAAGCTTCGGGTGTTGGACCCAGAGGTTACC 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 367 CAGCAGACCACAGAGCTCAAGGAAGAGTGCAAGGACTTTGTGGGCAAAATTGGCCAGTTT 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AshAlaSerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMet 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluLysLeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLys 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukāryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlnGlyLeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAla
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UI-M-CGOp-biq-b-11-0-UI.rl NIH_BMAP_Ret4_S2 Mus musculus cDNA clone UI-M-CGOp-biq-b-11-0-UI.s', mRNA sequence.
BM940927.1 GI:19400079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
Seq primer: M13 REVERSE.
                            105 GlnMetGluGluGlnSerLeuIleLysValLysGlyGluGln--------Glu 119
                                                                                                              85 ArgLysGlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluLeuGluArgLeu 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 691)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mEST@mail.nih.gov
Tissue Procurement: Dr. Xin-Yuan Fu, Yale University School of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
60892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                120 LeuMetIleGlnLysLeuSerAspSerSerSr 130
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Res. 6 (9), 791-806 (1996) 97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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Mus musculus
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Best Local Similarity:
Query Match:
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BM940927/c
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AUTHORS
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PUBMED
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /done_libs__NIA Mouse 15K cDNA Clone Set"
//done_libs__NIA Mouse 15K cDNA Clone Set"
//done_libs__NIA Mouse 15K cDNA Clone Set"
//done_libs__NIA Mouse 15K cDNA; Site_2: NotI; This clone is among a rearrayed set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfartilized egg to blastocyst, embryonic part of ET.5 embryos.
//doctored color of ET.5 embryos, extraembryonic part of ET.5 embryos, and EL2.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT) ovary cDNA library. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2)
Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5 day mouse embryos reveals enrichment in the t-complex and under-representation on the x chromosome, 1998, Hum Mol Genet 7: 1867-1978.
                                                                                                                             Please
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   534 CAGAAAATIGIIGGIGGICTAAITGAGCIIGIIGAICAGCIIGCCAAAGAAGCAGAAC 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        594 CAGCAGACTGTGGAGCTCAAGGAGGAGTGCAAGGACTTTGTGGACAAAATTGGCCAGTTT 535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 GlnGlyLeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAla 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 AsnAlaSerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMet 44
                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA
libraries"
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               Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
National Institute on Aging/National Institutes of Health
National Institute on Aging/National Institutes of Health
San Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. For the print thep://lgsun.grc.nia.nih.gov/cDNA/15k.html for details.
Plate: H3085 row: G column: 04
Seq primer: -21M13 Forward
High quality sequence stop: 687
POLYA-Yes.
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Matches:
Conservative:
Mismatches:
Indels:
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/db_xref="taxon:10090"
/clone="H3085G04"
                                                                                                                                                                                                                                                                           1. .687
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-866-582A-2 (1-135) x BG070290 (1-687)
                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="DH10B"
  Other_ESTs: H3085G04-5
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Best Local Similarity:
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/de_stage="Adult"
//de_stage="Adult"
//de_stage="Adult"
//de_stage="Adult"
//de_host="BHIDB (Life Technologies) (TI phage resistant)"
//clone_lib="NIH_BMAP_DJ2"
//note="Organ: brain; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-MD2 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is: GCTACATGAT, subfornical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H3136B04-3 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone H3136B04 3', mRNA sequence.
BG074519 GI:12557088
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 ArgLysGlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluLeuGluArgLeu 104
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Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 CGGGTTGAATATGAAGCTTTGTGTAAAGTAGAAGCAGAACAAAATGAATTTATTGACCAA 68
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/tissue_type="subfornical organ and postrema"
                                                                                                                                                                                                                                                                                                                                                                                        organ and area postrema.
TAG_LIB=UI-M-DJ2
TAG_TISSUE=subfornical organ and postrema
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BG074519/c
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ORIGIN
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UI-M-DJ2-bwa-p-16-0-UI.S1 NIH_BMAP_DJ2 Mus musculus cDNA clone
UI-M-DJ2-bwa-p-16-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mEST@mail.nih.gov
Tissue Procurement: Dr. Robin Davisson
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Seq primer: M13 FORWARD
POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                      GlnMetGluGluGluGlnSerLeuIleLysValLysGlyGluGln------Glu 119
                                                                                                                                                                                                                           ::: ||||
352 CAGCAGACTGTGGAGCTCAAGGAGGACTTTGTGGACAAATTGGCCAGTTT 293
                                                                                                                                                                                                                                                                                                                         85 ArgLysGlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluLeuGluArgLeu 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                             25 AsnAlaSerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMet 44
                                                                                                                                                                                                                                                                                           45 GlnGlyLeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAla 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 CGGGTTGAATATGAAGCTTTGTGTAAAGTAGAAGCAGAACAAAATGAATTTATTGACCAA 53
                                                                                                  AspargGlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyr 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD 20892-9643, USA
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National Institute of Mental Health
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Res. 6 (9), 791-806 (1996)
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          Gaps:
                                                     US-09-866-582A-2 (1-135) x BM940927 (1-691)
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Fax: 301 443 9890
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Mus musculus
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BQ177222/C DEFINITION

RESULT 49

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

AUTHORS TITLE

REFERENCE

MEDLINE PUBMED COMMENT

FEATURES

JOURNAL

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clone is among a rearrayed set of 15,247 clones from il
embryo cDNA libraries (including preimplantation stage
embryos from unfertilized egg to blastocyst, embryonic
part of ET.5 embryos, extraembryonic part of ET.5 embryos,
and EL2.5 female mesonephros/gonad) and one newborn
ovary cDNA library. Average insert size 1.5 kb. All
source libraries are cloned unidirectionally with oligo(dT)
)-Not primers. References include: (1) Genome-wide
expression profiling of mid-gestation placenta and embryo
using a 15,000 mouse developmental cDNA microarray,
Proc. Natl. Acad. Sci. U S A, 97: 91127-9132; (2)
Large-scale cDNA analysis reveals phased gene expression
patterns during preimplantation mouse development, 2000,
Development, 127: 1737-1749; (3) Genome-wide mapping of
unselected transcripts from extraembryonic tissue of
7.5-day mouse embryos reveals enrichment in the t-complex
and under representation on the X chromosome, 1998, Hum
Mol Genet 7: 1967-1978."
                                                                                                                                                                                                                                                                                         Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
National Institute on Aging/National Institutes of Health
Sacasell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
Visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details.
Seq primer: -21M13 Forward
High quality sequence stop: 775
POLYA=Yes.
               1 (bases 1.0 //),
Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X., Grahovac,M.J., Pantano,S., Sano,Y., Plao,Y., Nagaraja,R., Doi,H., Wood,W.H.
III, Becker,K.G. and Ko,M.S.H.
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                                                                                                            Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray Proc Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000) 20381348
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Matches:
Conservative:
Mismatches:
Indels:
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209 c 174 q
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90
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REFERENCE
AUTHORS
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289 CAGAAAATTGTTGGTGGTCTAATTGAGCTTGTTGATCAGCTTGCCAAAGAAGCAGAGAAC 230
                                                                                                                            229 GAGAAGATGAAGGCCATTGGTGCTCGGAACTTGCTGAAGTCCATAGCGAAGCAGAGAA 170
                                                                                                                                                                                           169 GCCCAGCAGCAGCTGCAGCCCTGATAGCAGAAAGAAGAGCAGCAAGAAAGTAT 110
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                                                                                                                                                                       85 ArgLysGlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluLeuGluArgLeu 104
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GlnGlyLeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAla
                                                                                   65 GluLysLeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLys
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